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TECH CENTER 1600/2900

11RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/555,704DATE: 03/14/2001
TIME: 10:48:34Input Set: A:\9150-0008.10-seqlist.txt
Output Set: N:\CRF3\03142001\I555704.raw

3 <110> APPLICANT: The Research Foundation for Microbial diseases of Osaka University
 5 <120> TITLE OF INVENTION: Japanese Encephalitis
 7 <130> FILE REFERENCE: P98AF308-2
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/555,704
 C--> 10 <141> CURRENT FILING DATE: 2000-06-02
 12 <160> NUMBER OF SEQ ID NOS: 4
 14 <170> SOFTWARE: PatentIn Ver. 2.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1500
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Japanese encephalitis virus
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (1)..(1500)
 25 <400> SEQUENCE: 1

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28	1 5 10 15	
30	gga gcc act tgg gtg gat ttg gtg tta gaa gga gat agt tgt ttg aca	96
31	Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Leu Thr	
32	20 25 30	
34	atc atg gca aac gac aaa cca aca cta gat gtc cgc atg atc aac att	144
35	Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val Arg Met Ile Asn Ile	
36	35 40 45	
38	gaa gct agc caa ctt gct gaa gtc agg agt tac tgc tat cac gct tca	192
39	Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr Cys Tyr His Ala Ser	
40	50 55 60	
42	gtc act gac att tca acg gtg gct cga tgc ccc acg act gga gaa gcc	240
43	Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala	
44	65 70 75 80	
46	cac aac gag aaa cgt gct gac agc agc tac gtg tgc aaa caa ggc ttt	288
47	His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val Cys Lys Gln Gly Phe	
48	85 90 95	
50	act gac cgc gga tgg gga aat gga tgt gga ctt ttc ggg aaa gga agc	336
51	Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser	
52	100 105 110	
54	att gac aca tgc gca aaa ttt tct tgt acc agt aag gcc att gga aga	384
55	Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser Lys Ala Ile Gly Arg	
56	115 120 125	
58	atg atc caa cca gag aac atc aag tac gag gtt ggc ata ttc gtg cac	432
59	Met Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val Gly Ile Phe Val His	
60	130 135 140	
62	ggg acc acc acc tcg gaa aac cat ggg aat tac tca gcg caa gta gga	480
63	Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr Ser Ala Gln Val Gly	
64	145 150 155 160	
66	gcg tct caa gca gca aag ttt act gta act cca aac gct ccc tca ata	528
67	Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro Asn Ala Pro Ser Ile	

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68		165		170		175	
70	acc ctc aag ctt ggt gat tat gga gag gtc aca ctg gat tgt gaa cca						576
71	Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr Leu Asp Cys Glu Pro						
72		180		185		190	
74	agg agt gga ctg aac act gaa gcg ttc tat gtc atg acc gtg ggt tcg						624
75	Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val Met Thr Val Gly Ser						
76		195		200		205	
78	aag tca ttc tta gtc cat agg gaa tgg ttc cat gac ctt tct ctt ccc						672
79	Lys Ser Phe Leu Val His Arg Glu Trp Phe His Asp Leu Ser Leu Pro						
80		210		215		220	
82	tgg acg tcc cct tca agc acg gca tgg agg aac aga gaa ctc ctc atg						720
83	Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn Arg Glu Leu Leu Met						
84	225		230		235	240	
86	gaa ttt gaa gag gca cat gcc aca aaa caa tct gtc gta gcc ctt ggg						768
87	Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser Val Val Ala Leu Gly						
88		245		250		255	
90	tca cag gag gga ggc ctc cat caa gcg ttg gca gga gcc atc gtg gtg						816
91	Ser Gln Glu Gly Leu His Gln Ala Leu Ala Gly Ala Ile Val Val						
92		260		265		270	
94	gag tac tcg agc tca gtg aag tta aca tca ggt cac ctg aaa tgc agg						864
95	Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg						
96		275		280		285	
98	cta aaa atg gac aaa ctg gct ctg aag ggc acg act tat ggc atg tgt						912
99	Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr Thr Tyr Gly Met Cys						
100		290		295		300	
102	aca gaa aaa ttc tcg ttc gcg aaa aat cca gcg gac aca ggc cat gga						960
103	Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala Asp Thr Gly His Gly						
104	305		310		315	320	
106	aca gtt gtc att gag ctc aca tat tct gga agc gat ggc tcc tgt aaa						1008
107	Thr Val Val Ile Glu Leu Thr Tyr Ser Gly Ser Asp Gly Ser Cys Lys						
108		325		330		335	
110	att ccg att gtc tca gtt gcg agc ctc aat gac atg acc cct gtg ggg						1056
111	Ile Pro Ile Val Ser Val Ala Ser Leu Asn Asp Met Thr Pro Val Gly						
112		340		345		350	
114	agg ctg gta aca gta aac ccc ttc gtt gcg aca tct agc tcc aac tca						1104
115	Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Ser Ser Asn Ser						
116		355		360		365	
118	aag gtg ctg gtt gag atg gaa cct ccc ttc gga gac tct tat atc gtg						1152
119	Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val						
120		370		375		380	
122	gtt gga aga ggg gac aag cag att aac cat cac tgg cac aaa gct gga						1200
123	Val Gly Arg Gly Asp Lys Gln Ile Asn His His Trp His Lys Ala Gly						
124	385		390		395	400	
126	agc acg ctg ggc aaa gcc ttc tca aca act ttg aaa ggg gct cag aga						1248
127	Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg						
128		405		410		415	
130	tta gca gcg cta ggt gac aca gcc tgg gac ttc ggc tcc att gga ggg						1296
131	Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly						
132		420		425		430	

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134 gta ttc aac tcc ata ggg aaa gct gtt cac caa gta ttt ggc ggt gca 1344
135 Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
136      435      440      445
138 ttc aga acg ctc ttt ggg gga atg tct tgg atc aca caa gga cta atg 1392
139 Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met
140      450      455      460
142 ggg gcc ttg ctt ctt tgg atg ggt gtc aac gca cga gac cgg tca atc 1440
143 Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile
144 465      470      475      480
146 gcc ctg gct ttt ttg gcc acg gga ggt gtg ctc gtg ttt tta gcg acc 1488
147 Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr
148      485      490      495
150 aat gtg cat gcc / 1500
151 Asn Val His Ala
152      500
155 <210> SEQ ID NO: 2
156 <211> LENGTH: 500
157 <212> TYPE: PRT
158 <213> ORGANISM: Japanese encephalitis virus
160 <400> SEQUENCE: 2
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163 1      5      10      15
165 Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Leu Thr
166      20      25      30
168 Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val Arg Met Ile Asn Ile
169      35      40      45
171 Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr Cys Tyr His Ala Ser
172      50      55      60
174 Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala
175 65      70      75      80
177 His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val Cys Lys Gln Gly Phe
178      85      90      95
180 Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
181      100      105      110
183 Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser Lys Ala Ile Gly Arg
184      115      120      125
186 Met Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val Gly Ile Phe Val His
187      130      135      140
189 Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr Ser Ala Gln Val Gly
190 145      150      155      160
192 Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro Asn Ala Pro Ser Ile
193      165      170      175
195 Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr Leu Asp Cys Glu Pro
196      180      185      190
198 Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val Met Thr Val Gly Ser
199      195      200      205
201 Lys Ser Phe Leu Val His Arg Glu Trp Phe His Asp Leu Ser Leu Pro
202      210      215      220
204 Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn Arg Glu Leu Leu Met

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207 Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser Val Val Ala Leu Gly
208          245          250          255
210 Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala Gly Ala Ile Val Val
211          260          265          270
213 Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
214          275          280          285
216 Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr Thr Tyr Gly Met Cys
217          290          295          300
219 Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala Asp Thr Gly His Gly
220 305          310          315          320
222 Thr Val Val Ile Glu Leu Thr Tyr Ser Gly Ser Asp Gly Ser Cys Lys
223          325          330          335
225 Ile Pro Ile Val Ser Val Ala Ser Leu Asn Asp Met Thr Pro Val Gly
226          340          345          350
228 Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr Ser Ser Asn Ser
229          355          360          365
231 Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
232          370          375          380
234 Val Gly Arg Gly Asp Lys Gln Ile Asn His His Trp His Lys Ala Gly
235 385          390          395          400
237 Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg
238          405          410          415
240 Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
241          420          425          430
243 Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
244          435          440          445
246 Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met
247          450          455          460
249 Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile
250 465          470          475          480
252 Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr
253          485          490          495
255 Asn Val His Ala
256          500
259 <210> SEQ ID NO: 3
260 <211> LENGTH: 1500
261 <212> TYPE: DNA
262 <213> ORGANISM: Japanese encephalitis virus
264 <220> FEATURE:
265 <221> NAME/KEY: CDS
266 <222> LOCATION: (1)..(1500) /
268 <400> SEQUENCE: 3
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270 Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe Ile Glu Gly Ala Ser
271 1 5 10 15
273 gga gcc act tgg gtg gac ttg gtg cta gaa gga gac agc tgc ttg aca 96
274 Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Leu Thr
275 20 25 30

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277 atc atg gca aac gac aaa cca aca ttg gac gtc cgc atg atc aac atc 144
278 Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val Arg Met Ile Asn Ile
279          35          40          45
281 gaa gct agc caa ctt gct gag gtc aga agt tac tgc tat cat gct tca 192
282 Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr Cys Tyr His Ala Ser
283          50          55          60
285 gtc act gac atc tcg acg gtg gct cgg tgc ccc acg act gga gaa gcc 240
286 Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala
287          65          70          75          80
289 cac aac gag aag cga gct gat agt agc tat gtg tgc aaa caa ggc ttc 288
290 His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val Cys Lys Gln Gly Phe
291          85          90          95
293 act gat cgt ggg tgg ggc aac gga tgt gga ctt ttc ggg aag gga agt 336
294 Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
295          100          105          110
297 att gac aca tgt gca aaa ttc tcc tgc acc agg aaa gcg att ggg aga 384
298 Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Arg Lys Ala Ile Gly Arg
299          115          120          125
301 aca atc cag cca gaa aac atc aaa tac gaa gtt ggc att ttt gtg cat 432
302 Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val Gly Ile Phe Val His
303          130          135          140
305 gga acc acc act tcg gaa aac cat ggg aat tat tca gcg caa gtt ggg 480
306 Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr Ser Ala Gln Val Gly
307          145          150          155          160
309 gcg tcc cag gcg gca aag ttt aca gta aca cct aat gct cct tcg ata 528
310 Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro Asn Ala Pro Ser Ile
311          165          170          175
313 acc ctc aaa ctt ggt gac tac gga gaa gtc aca ctg gac tgt gag cca 576
314 Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr Leu Asp Cys Glu Pro
315          180          185          190
317 agg agt gga cta aac act gaa gcg ttt tac gtc atg acc gtg ggg tca 624
318 Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val Met Thr Val Gly Ser
319          195          200          205
321 aag tca ttt ttg gtc cat agg gaa tgg ttt cat gac ctc gct ctc cct 672
322 Lys Ser Phe Leu Val His Arg Glu Trp Phe His Asp Leu Ala Leu Pro
323          210          215          220
325 tgg acg ccc cct tcg agc aca gcg tgg aga aac aga gaa ctc ctc atg 720
326 Trp Thr Pro Pro Ser Ser Thr Ala Trp Arg Asn Arg Glu Leu Leu Met
327          225          230          235          240
329 gaa ttt gaa gag gcg cac gcc aca aaa cag tcc gtt gtt gct ctt ggg 768
330 Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser Val Val Ala Leu Gly
331          245          250          255
333 tca cag gaa gga ggc ctc cat cag gcg ttg gca gga gcc atc gtg gtg 816
334 Ser Gln Glu Gly Leu His Gln Ala Leu Ala Gly Ala Ile Val Val
335          260          265          270
337 gag tac tca agc tca gtg aag tta aca tca ggc cac cta aaa tgc agg 864
338 Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
339          275          280          285
341 ctg aaa atg gac aaa ctg gct ctg aaa ggc aca acc tat ggt atg tgc 912

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VERIFICATION SUMMARY

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TIME: 10:48:36

Input Set : A:\9150-0008.10-seqlist.txt

Output Set: N:\CRF3\03142001\I555704.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date